

acc taa gac agc gga cca gac ggc acc cca gac acc gtc tac agc atc Thr Trp Asp Ser Gly Pro Glu Gly Thr Pro Asp Thr Val Tyr Ser Ile 40 45 50 55	198
gag tat aag acg tac gga gag agg gac tgg gtg gca aag aag ggc tgt Glu Tyr Lys Thr Tyr Gly Glu Arg Asp Trp Val Ala Lys Lys Gly Cys 60 65 70	246
cag cgg atc acc cgg aag tcc tgc aac ctg acg gtg gag aag ggc aac Gln Arg Ile Thr Arg Lys Ser Cys Asn Leu Thr Val Glu Thr Gly Asn 75 80 85	294
ctc acg gag ctc tac tat gcc agg gtc acc gct gtc aat ggc gga ggc Leu Thr Glu Leu Tyr Tyr Ala Arg Val Thr Ala Val Ser Ala Gly Gly 90 95 100	342
cgg tca gcc acc aag atg act gac agg ttc agc tct ctg cag cac act Arg Ser Ala Thr Lys Met Thr Asp Arg Phe Ser Ser Leu Gln His Thr 105 110 115	390
acc ctc aag cca cct gat gtg acc tgt atc tcc aaa gtg aga tgg att Thr Leu Lys Pro Pro Asp Val Thr Cys Ile Ser Lys Val Arg Ser Ile 120 125 130 135	438
cag atg att gtt cat cct acc ccc acg cca atc cgt gca ggc gat ggc Gln Met Ile Val His Pro Thr Pro Thr Pro Ile Arg Ala Gly Asp Gly 140 145 150	486
cac cgg cta acc ctg gaa gac atc ttc cat gac ctg ttc tac cac tta His Arg Leu Thr Leu Glu Asp Ile Phe His Asp Leu Phe Tyr His Leu 155 160 165	534
gag ctc cag gtc aac cgc acc tac caa atg cac ctt gga ggc aag cag Glu Leu Gln Val Asn Arg Thr Tyr Gln Met His Leu Gly Gly Lys Gln 170 175 180	582
aga gaa tat gag ttc ttc ggc ctg acc cct gac aca gag ttc ctt ggc Arg Glu Tyr Glu Phe Phe Gly Leu Thr Pro Asp Thr Glu Phe Leu Gly 185 190 195	630
acc atc ata att tgc att ccc acc tga gcc aag aag aat acc ccc tac 678	

Thr Thr Met Thr Val Val Thr Thr Thr Ala Val Ala Ser Ala Thr Thr	200	205	210	215
atg tac cca att cca aca cta cca cca cca cca tgg ac cca tta ttt	220	225	230	235
Met Lys Ala Val Lys Thr Leu Pro Asp Arg Thr Trp Thr Tyr Ser Phe				
tcc gga acc ttc cta ttt tcc tcc atg acc ttc cta gtc gaa gta cta tta	235	240	245	250
Ser Gly Ala Phe Trp Pro Ser Met Gly Phe Leu Val Ala Val Leu Lys				
tac cta acc tac aca tat gtc acc aac cca cta gaa cct cca aac tta	255	260	265	270
Tyr Leu Ser Tyr Arg Tyr Val Thr Lys Pro Pro Ala Pro Phe Asn Ser				
ctg aac gtc cca cca gtc ctg act ttc cca cca ctg cca tta ata cca	265	270	275	280
Leu Asn Val Gln Arg Val Leu Thr Phe Gln Pro Leu Arg Phe Ile Gln				
gag cac gtc cta ata cct gtc ttt gac ctc agc ggc ccc aac agt ctg	280	285	290	295
Glu His Val Leu Ile Pro Val Phe Asp Leu Ser Gly Pro Ser Ser Leu				
gcc caa cct gtc caa tac tcc caa atc aag ctg tct gga ccc aag caa	300	305	310	315
Ala Gln Pro Val Gln Tyr Ser Gln Ile Arg Val Ser Gly Pro Arg Glu				
ccc gca qga gct cca cag cgg cat agc ctg tcc gag atc acc tac tta	315	320	325	330
Pro Ala Gly Ala Pro Gln Arg His Ser Leu Ser Glu Ile Thr Tyr Leu				
ggg caa cca gac att tcc atc ctc cag ccc tcc aac gtc cca cct ccc	330	335	340	345
Gly Gln Pro Asp Ile Ser Ile Leu Gln Pro Ser Asn Val Pro Pro Pro				
cag atc ctc tcc cca cta tcc tat ggc cca aac gct acc ctt gaa atc	345	350	355	360
Gln Ile Leu Ser Pro Leu Ser Tyr Ala Pro Asn Ala Ala Pro Glu Val				
gag ccc cca tta tta cca cta cta acc cca gaa gct cca tta cca	365	370	375	380
Gly Pro Pro Ser Tyr Ala Pro Gln Val Thr Pro Glu Ala Gln Phe Pro				

ttt tac ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt	1236
Phe Tyr Ala Pro Gln Ala Thr Ser Tyr Val Gln Pro Ser Ser Tyr Ala	
385 390	
ccg caa gcc act cca aa gac tgg ctt ccc tcc tat agg gta tgc atg	1254
Pro Gln Ala Thr Pro Asp Ser Trp Pro Pro Ser Tyr Gly Val Cys Met	
395 400 405	
gaa ggt tct ggc aat gaa gac ccc act gga aca ctt tct agt cct aat	1302
Glu Gly Ser Gly Tyr Asp Ser Pro Thr Gly Thr Leu Ser Ser Pro Tyr	
410 415 420	
cac ctt agg ctt aat aat cag ctt cag aaa aag cca cca act gga agc	1350
His Leu Arg Pro Tyr Gly Gln Leu Gln Tyr Glu Pro Pro Ala Gly Ser	
425 430 435	
tgc atg tta ggt ggc ctt tct ctg caa gag ctg acc tcc ttg gct atg	1398
Cys Met Leu Gly Gly Leu Ser Leu Gln Glu Val Thr Ser Leu Ala Met	
440 445 450 455	
gag gaa tcc caa gaa gca aaa tca ttg cac cag ccc ctg ggg att tgc	1446
Glu Glu Ser Gln Glu Ala Lys Ser Leu His Gln Pro Leu Gly Ile Cys	
460 465 470	
aca gac aga aca tct gac cca aat gtg cta cac agt ggg gag gaa ggg	1494
Thr Asp Arg Thr Ser Asp Pro Asn Val Leu His Ser Gly Glu Glu Gly	
475 480 485	
aca cca cag tac cta aag ggc cag ctg ccc ctg ctg tcc tca gtc cag	1542
Thr Pro Gln Tyr Leu Tyr Gly Gln Leu Pro Leu Leu Ser Ser Val Gln	
490 495 500	
atc gag ggc cac ccc atg tcc ctg cct ttg caa cct cct tcc ggt cca	1590
Ile Glu Gly His Pro Met Ser Leu Pro Leu Gln Pro Pro Ser Gly Pro	
505 510 515	
tgt tcc ccc tca gaa caa aat cca aat ccc tga ggc ctg ctg gag tcc	1638
Cys Ser Pro Ser Arg Gln Gly Pro Ser Pro Trp Gly Leu Leu Glu Ser	
520 525 530 535	
ctt atg tat cca aat aat aaa gcc aat agc cca acc ctt gag acc tca	1686
Leu Val Tyr Pro Tyr Arg Glu Ala Lys Ser Pro Ala Pro Glu Thr Ser	
540 545 550	

gac cta gaa cag cca cca cca cca gat tat ctt ttt cca ggc ctg gca 1764
 Asp Leu Glu Gln Pro Thr Ala Leu Asp Ser Leu His Arg Gly Leu Ala
 555 560 565

ctg act gtg cag tgg gaa ttc tgaaggggaat gggaaaagct tgggtgcttc 1785
 Leu Thr Val Gln Trp Glu Ser
 570

ttcctatccc taaccagtat caccatcttg gctgtcaatc ccattgctgc ccattgccaca 1845
 cactctgaga tatggctca caccattgcc cttgagagaa acagaaggaa tggcatgag 1905
 gcccctgccc atgagtgagc tctcaccg aacaaagcag catgataagg actgcagcgg 1965
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<211> 574

<212> PRT

<213> Homo sapien

<400> 2

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 20 25 30
 Ser Asn Phe Glu Asn Ile Leu Thr Trp Asp Ser Gly Pro Glu Gly Thr
 35 40 45
 Pro Asp Thr Val Tyr Ser Ile Glu Tyr Lys Thr Tyr Gly Glu Arg Asp
 50 55 60

Trp Val Ala Leu Val Ser Val Ala Thr Thr Arg Val Ser Val Arg
 85 90 95 100 105 110 115 120 125 130
 Leu Thr Val Val Thr Val Arg Leu Thr Val Leu Tyr Tyr Ala Arg Val
 135 140 145 150 155 160 165 170 175 180
 Thr Ala Val Ser Ala Gly Gly Arg Ser Ala Thr Lys Met Thr Asp Arg
 185 190 195 200 205 210 215 220 225 230
 Phe Ser Ser Leu Gln His Thr Thr Leu Lys Pro Pro Asp Val Thr Cys
 235 240 245 250 255 260 265 270 275 280
 Ile Ser Lys Val Arg Ser Ile Gln Met Thr Val His Pro Thr Pro Thr
 285 290 295 300 305 310 315 320 325 330
 Pro Ile Arg Ala Gly Asp Gly His Arg Leu Thr Leu Glu Asp Ile Phe
 335 340 345 350 355 360 365 370 375 380
 His Asp Leu Phe Tyr His Leu Glu Leu Gln Val Asn Arg Thr Tyr Gln
 385 390 395 400 405 410 415 420 425 430
 Met His Leu Gly Gly Lys Gln Arg Glu Tyr Glu Phe Phe Gly Leu Thr
 435 440 445 450 455 460 465 470 475 480
 Pro Asp Thr Glu Phe Leu Gly Thr Ile Met Ile Lys Val Pro Thr Trp
 485 490 495 500 505 510 515 520 525 530
 Ala Lys Glu Ser Ala Pro Tyr Met Cys Arg Val Lys Thr Leu Pro Asp
 535 540 545 550 555 560 565 570 575 580
 Arg Thr Trp Thr Tyr Ser Phe Ser Gly Ala Phe Leu Phe Ser Met Gly
 585 590 595 600 605 610 615 620 625 630
 Phe Leu Val Ala Val Leu Cys Tyr Leu Ser Tyr Arg Tyr Val Thr Lys
 635 640 645 650 655 660 665 670 675 680
 Pro Pro Ala Pro Pro Asn Ser Leu Asn Val Gln Arg Val Leu Thr Phe
 685 690 695 700 705 710 715 720 725 730
 Gln Pro Leu Arg Phe Ile Gln Glu His Val Leu Ile Pro Val Phe Asp
 735 740 745 750 755 760 765 770 775 780
 Leu Ser Gly Pro Ser Ser Leu Ala Gln Pro Val Gln Tyr Ser Gln Ile
 785 790 795 800 805 810 815 820 825 830
 Arg Val Ser Gly Pro Arg Glu Pro Ala Gly Ala Pro Gln Arg His Ser
 835 840 845 850 855 860 865 870 875 880
 Leu Ser Glu Ile Thr Tyr Leu Gly Gln Pro Asp Ile Ser Ile Leu Gln
 885 890 895 900 905 910 915 920 925 930
 Pro Ser Asn Val Pro Pro Pro Gln Ile Leu Ser Pro Leu Ser Tyr Ala
 935 940 945 950 955 960 965 970 975 980
 Pro Asn Ala Ala Pro Gln Val Gly Pro Pro Ser Tyr Ala Pro Gln Val
 985 990 995 1000 1005 1010 1015 1020 1025 1030
 Thr Pro Glu Ala Gln Phe Pro Phe Tyr Ala Pro Gln Ala Ile Ser Lys
 1035 1040 1045 1050 1055 1060 1065 1070 1075 1080
 Val Gln Pro Ser Ser Tyr Ala Pro Gln Ala Thr Pro Asp Ser Trp Trp
 1085 1090 1095 1100 1105 1110 1115 1120 1125 1130

Val	Val	Val	Val	Val	Met	Ala	Val	Val	Val	Val	Pro	Leu	
			415				41					415	
Gly	Pro	Leu	Val	Val	Val	Val	Leu	Arg	Val	Val	Gln	Leu	Glu
			425				425					430	
Lys	Glu	Pro	Pro	Ala	Val	Val	Met	Leu	Gly	Gly	Leu	Ser	Leu
			435				440					445	
Glu	Val	Thr	Ser	Leu	Ala	Met	Ala	Glu	Ser	Gln	Glu	Ala	Lys
			450			455							
His	Glu	Pro	Leu	Gly	Thr	Lys	Thr	Asp	Arg	Thr	Ser	Asp	Pro
			465			470				475			480
Leu	His	Ser	Gly	Gln	Gln	Gly	Thr	Pro	Gln	Lys	Leu	Lys	Gly
			485						490				495
Pro	Leu	Leu	Ser	Ser	Val	Gln	Ile	Glu	Gly	His	Pro	Met	Ser
			500						505				510
Leu	Gln	Pro	Pro	Ser	Gly	Pro	Lys	Ser	Pro	Ser	Asp	Gln	Gly
			515				520					525	
Pro	Trp	Gly	Leu	Leu	Ala	Ser	Leu	Val	Lys	Pro	Lys	Asp	Glu
			530				535					540	
Ser	Pro	Ala	Pro	Gln	Thr	Ser	Asp	Leu	Glu	Gln	Pro	Thr	Glu
			545			550				555			560
Ser	Leu	Phe	Arg	Gly	Leu	Ala	Leu	Thr	Val	Gln	Trp	Glu	Ser
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<210> 3

$\langle 211 \rangle$ 211

<212> PPT

-213- Hum. Capital

<.100> 3

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Asp Thr Val Tyr Ser Thr Ala Tyr Lys Thr Tyr Gly Glu Arg Asp Trp
35 40 45
Val Ala Tyr Cys Gly Cys Glu Gln Ser Ile Thr Arg Leu Ser Cys Asn Leu
50 55 60
Thr Val Ala Thr Gly Ser Leu Trp Glu Leu Tyr Tyr Ala Arg Val Thr
65 70 75 80
Ala Val Ser Gly Gly Thr Ser Ala Thr Val Met Thr Asp Arg Phe
85 90 95

Ser Ser Leu Gln Met His Thr Ser Lys Pro Pro Asp Val Thr Tyr Ile
 110
 Ser Lys Val Arg Ser Ile Gln Met Ile Val His Pro Thr Pro Thr Pro
 115
 Ile Arg Ala Gly Asp Gly His Arg Leu Thr Leu Glu Asp Ile Phe His
 120
 130 135 140
 Asp Leu Phe Tyr His Leu Glu Leu Gln Val Asn Arg Thr Tyr Gln Met
 145 150 155 160
 His Leu Gly Gly Lys Gln Arg Glu Tyr Glu Phe Phe Gly Leu Thr Pro
 165 170 175
 Asp Thr Glu Thr Leu Gly Thr Ile Met Ile Cys Val Pro Thr Trp Ala
 180 185 190
 Lys Glu Ser Ala Pro Tyr Met Cys Arg Val Lys Thr Leu Pro Asp Arg
 195 200 205
 Thr Trp Thr
 210

<210> 4

<211> 6

<212> PRI

<213> Artificial Sequence

<220>

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<400> 4

Glu Tyr Met Pro Met Glu

1

5

<210> 5

<211> 8

<212> PRI

<213> Artificial Sequence

<220>

<223> Flag tag peptide

<400> 5

Asp Tyr Lys Arg Asp Asp Asp Lys

1

5

<10> 6

<11> 699

<12> DNA

<13> Homo sapiens

<400> 6

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acccctgagg tcaatqacgt ggtgggtggac gtgagccacg aagacccatga ggtcaagttc      180
aactcgtacg tgaacnqgt ggaggtcat aatgcacaga caaagccgcc ggaggaagag      240
tacaacagca cgtaccgtgt ggtcagcgtc ctaccctcc tgcaccagga ctgctgaat      300
qqcaaggagt ac aagtgcac ggtctccaac aaagccctcc catctccat cgaagaaaac      360
ttctccaaq ccaagggca gccccagaga ccacaggtgt acaccctgcc cccatccgg      420
gatgagtgta ccaagaacca ggtcagcgtg acctgcctgg tcaagagctt ctatccagc      480
gacatccgcg tggagtgga gagcaatggg cagccggaga acaactacaa gaccacgct      540
cccgtgtgg actccgacgg ctctttctt ctctacagca agctcaccgt ggacaagagc      600
aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac      660
tacaagcaga agagcctctc cctgtctccg ggtaaataa      699

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<10> 7

<11> 1116

<12> DNA

<13> homo sapiens

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<11> CDS

<12> (21)...(557)

<400> 7

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                               Met Ala Ala Leu Gln Lys Ser Val Ser Ser Phe
                               1           5           10

cct atg ggg acc ctg gcc acc agc tgc ctg ctt ctg ttg gcc ctg ttg      101
Leu Met Gly Thr Leu Ala Thr Ser Cys Leu Leu Leu Leu Ala Leu Leu
           15           20           25

gta cag gga gga gga gct ggg ccc atc agc tcc cac tgc agg ctt gac      149
Val Gln Gly Gly Ala Ala Ala Pro Ile Ser Ser His Cys Arg Leu Asp
           30           35           40

agg tcc aac ttc cgt cgt ccc tat atc aac cag acc ttc atg ttg      197

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Lys Ser Asn Phe Gln Gln Pro Tyr Ile Thr Asn Arg Thr Phe Met Leu
45 50 55

gct aag gag gct aac tta gct cat aac aac aca gac gtt cgt ctc att 245
Ala Lys Glu Ala Ser Leu Ala Asp Asn Asn Thr Asp Val Arg Leu Ile
60 65 70 75

ggg gag aaa ctg ttc cac gga gtc agt atg agt gag cgc tgc tat ctg 293
Gly Glu Lys Leu Phe His Gly Val Ser Met Ser Glu Arg Cys Tyr Leu
80 85 90

atg aag cag gtg ctg aac ttc acc ctt gaa gaa gtg ctg ttc cct caa 341
Met Lys Gln Val Leu Asn Phe Thr Leu Glu Glu Val Leu Phe Pro Gln
95 100 105

tct gat agg ttc cag cct tat atg cag gag gtg gtg ccc ttc ctg gcc 389
Ser Asp Arg Phe Gln Pro Tyr Met Gln Glu Val Val Pro Phe Leu Ala
110 115 120

agg ctg agc aac agg cta agc aca tgt cat att gaa ggt gat gac ctg 437
Arg Leu Ser Asn Arg Leu Ser Thr Cys His Ile Glu Gly Asp Asp Leu
125 130 135

cat atc cag agg aat gtg caa aag ctg aag gac aca gtg aaa aag ctt 485
His Ile Gln Arg Asn Val Gln Lys Leu Lys Asp Thr Val Lys Lys Leu
140 145 150 155

gga gag agt gga gag atc aaa gca att gga gaa ctg gat ttg ctg ttt 533
Gly Glu Ser Gly Glu Ile Lys Ala Ile Gly Glu Leu Asp Leu Leu Phe
160 165 170

atg tct ctg aga aat acc tgc att tgaccagagc aaagctgaaa aatgaataac 567
Met Ser Leu Arg Asn Ala Cys Ile
175

aaacccctt tontgtatg aaataacaat tagatcccc aaagcattt ttittaanca 647
aaaggaagat ggaagacaa actccatcat gatggatgga ttccaaatga acccttggt 707
taattacaa ggaacacaa gccactttt ttataagac gagaaggtag attttctaa 767
catagatatt tattgataac atttcattgt aactggtatt ctatacaca aaaacaattt 827
atttttttaa taattgtctt ttccataaaa aaagattact ttccattcct ttaggggaaa 887
aaacccctaa atagcttcat gtttccataa taagtacttt atatttataa atgtatttat 947
tattattata aaactgcatt ttatttatat catittatta atatgaattt atttataaaa 1007
acatcatttg atattgtac tttaatttaa gactaattat tatatttata acaataatta 1067

1 1 1 1

1111

21. PRI

<213> homo sapiens

<400> 8

[illegible]

210-9

• 211 • 36

<212> DNA

• 213 • Artificial Sequence

• 20 •

223 Phosphonucleotide primer 3,38590

• 10 •

<400> 13
 His His His His His His
 1 5

<210> 14
 <211> 63
 <212> DNA
 <213> Artificial Sequence

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 <23> Oligonucleotide primer ZC29239

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 ttc 63

<210> 15
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 <212> DNA
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 gggag 65

<210> 16
 <211> 37
 <212> DNA
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<210> 17
 <211> 28
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<210> Amino acid sequence

<211>

<212> Other nucleotide primer (5'-3')

<400> 17

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28

<210> 18

<211> 660

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(660)

<400> 18

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1 5 10 15

48

gca ttg gga atg gta cca cct ccc gaa aat gtc aga atg aat tct gtt
Ala Leu Gly Met Val Pro Pro Pro Glu Asn Val Arg Met Asn Ser Val
20 25 30

96

aat ttc aag aac att cta cag tgg gag tca cct gct ttt gcc aaa ggg
Asn Phe Lys Asn Ile Leu Gln Trp Glu Ser Pro Ala Phe Ala Lys Gly
35 40 45

144

aac ctg act ttc aca gct cag tac cta agt tat agg ata ttc caa gat
Asn Leu Thr Phe Thr Ala Gln Tyr Leu Ser Tyr Arg Ile Phe Gln Asp
50 55 60

192

aaa tgc atg aat act acc ttg acg gaa tgt gat ttc tca aat ctt tcc
Lys Cys Met Asp Thr Thr Leu Thr Glu Cys Asp Phe Ser Ser Leu Ser
65 70 75 80

240

aag tat aat gac cac acc ttg aag gtc aag act gaa ttt gca gat gaa
Lys Tyr Glu Asp His Thr Leu Arg Val Arg Ala Glu Phe Ala Asp Glu
85 90 95

288

cat tgc att ttt gta ggc att tgc ttt ttt ttt ttt ttt ttt ttt ttt

336

Phe Ser Arg Thr Val Arg Ile Thr Glu Val Pro Val Asp Arg Thr Ile
10 15 20 25 30 35 40 45 50 55 60 65

att gga ccc cct gaa atg caa ata gaa ata ctt gat gat tat tta cat 384
Ile Gly Pro Pro Gly Met Gln Val Ala Val Leu Asp Asp Ser Leu His
115 120 125

atg cgt ttc tta gcc cct aaa att gag aat gaa tac gaa act tgg act 432
Met Arg Phe Leu Ala Pro Lys Ile Glu Asn Glu Tyr Glu Thr Trp Thr
130 135 140

atg aag aat gtg tat aac tca tgg act tat aat gtg caa tac tgg aaa 480
Met Lys Asn Val Tyr Asn Ser Trp Thr Tyr Asn Val Gln Tyr Trp Lys
145 150 155 160

aac ggt act gat gaa aag ttt caa att act ccc cag tat gac ttt gag 528
Asn Gly Thr Asp Glu Lys Phe Gln Ile Thr Pro Gln Tyr Asp Phe Glu
165 170 175

gtc ctc aga aac ctg gag cca tgg aca act tat tgt gtt caa gtt cga 576
Val Leu Arg Asn Leu Glu Pro Trp Thr Thr Tyr Cys Val Gln Val Arg
180 185 190

ggg ttt ctt cct gat cgg aac aaa gct ggg gaa tgg agt gag cct gtc 624
Gly Phe Leu Pro Asp Arg Asn Lys Ala Gly Glu Trp Ser Glu Pro Val
195 200 205

tgt gag caa aca acc cat gac gaa acg gtc ccc tcc 660
Cys Glu Gln Thr Thr His Asp Glu Thr Val Pro Ser
210 215 220

<210> 19

<211> 230

<212> PRT

<213> Homo sapiens

<400> 19

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Ala Leu Gly Met Val Pro Pro Pro Glu Asn Val Arg Met Asn Ser Val
20 25 30 35 40 45 50 55 60

Asn Phe Lys Asn Ile Leu Thr Trp Glu Ser Pro Ala Phe Ala Lys Gly
 35 40 45
 Asn Leu Thr Phe Thr Ala Val Tyr Leu Ser Tyr Arg Ile Phe Gln Asp
 50 55 60
 Lys Lys Met Asn Thr Thr Leu Thr Glu Cys Asp Phe Ser Ser Leu Ser
 65 70 75 80
 Lys Tyr Gly Asp His Thr Leu Arg Val Arg Ala Glu Phe Ala Asp Glu
 85 90 95
 His Ser Asp Trp Val Asn Ile Thr Phe Cys Pro Val Asp Asp Thr Ile
 100 105 110
 Ile Gly Pro Pro Gly Met Gln Val Glu Val Leu Asp Asp Ser Leu His
 115 120 125
 Met Arg Phe Leu Ala Pro Lys Ile Glu Asn Glu Tyr Glu Thr Trp Thr
 130 135 140
 Met Lys Asn Val Tyr Asn Ser Trp Thr Tyr Asn Val Gln Tyr Trp Lys
 145 150 155 160
 Asn Gly Thr Asp Glu Lys Phe Gln Ile Thr Pro Gln Tyr Asp Phe Glu
 165 170 175
 Val Leu Arg Asn Leu Glu Pro Trp Thr Thr Tyr Cys Val Gln Val Arg
 180 185 190
 Gly Phe Leu Pro Asp Arg Asn Lys Ala Gly Glu Trp Ser Glu Pro Val
 195 200 205
 Cys Glu Gln Thr Thr His Asp Glu Thr Val Pro Ser
 210 215 220

<210> 20

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer J038931

<400> 20

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18

<210> 21

<211> 82

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer (5'-end)

<400> 21

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gtttacctgg agacagggag ag 82

<10> 22

<11> 1428

<12> DNA

<13> Artificial Sequence

<20>

<21> CDS

<22> (1)...(1428)

<23> CRF2-4 extracellular cytokine binding domain fused
to IgG1 with a 6-HIS tag

<400> 22

atg ggg tgg agt ctt ggg agc tgg ctg ggt ggc tgc ctg ctg gtg tca 48
Met Ala Trp Ser Leu Gly Ser Trp Leu Gly Gly Cys Leu Leu Val Ser
1 5 10 15

gaa ttg gga atg gta cca cct ccc gaa aat gtc aga atg aat tct gtt 96
Ala Leu Gly Met Val Pro Pro Pro Glu Asn Val Arg Met Asn Ser Val
20 25 30

aat ttc aag aac att cta cag tgg gag tca cct gct ttt gcc aaa ggg 144
Asn Phe Lys Asn Ile Leu Gln Trp Glu Ser Pro Ala Phe Ala Lys Gly
35 40 45

aac ctg act ttc aca gct cag tac cta agt tat agg ata ttc caa gat 192
Asn Leu Thr Phe Thr Ala Gln Tyr Leu Ser Tyr Arg Ile Phe Gln Asp
50 55 60

aaa tgc atg aat act acc ttg acg gaa tat gat ttc tca agt ctt tcc 240
Lys Cys Met Asn Thr Thr Leu Thr Glu Cys Asp Phe Ser Ser Leu Ser
65 70 75 80

aag tat ggt gac cgc acc tta aga gtc aag gct gaa ttt gaa gat gag 288
Lys Tyr Gly Asp His Thr Leu Arg Val Arg Ala Glu Phe Ala Asp Glu
85 90 95

cat tca gac tga cta tca tca ttc tgt ctt att tat tac acc att Ser Asp Trp Val Asn Ile Thr Phe Cys Pro Val Asp Asp Thr Ile 100 105 110	336
att gga ccc cct gga atg caa gta gaa gta ctt gat gat tct tta cat Ile Gly Pro Pro Gly Met Gln Val Glu Val Leu Asp Asp Ser Leu His 115 120 125	384
atg cgt ttc tta gtc cct aaa att gag aat gaa tac caa act tgg act Met Arg Phe Leu Ala Pro Lys Ile Glu Asn Glu Tyr Glu Thr Trp Thr 130 135 140	432
atg aag aat gtg tat aac tca tgg act tat aat gtg caa tac tgg aaa Met Lys Asn Val Tyr Asn Ser Trp Thr Tyr Asn Val Glu Tyr Trp Lys 145 150 155 160	480
aac ggt act gat gaa aag ttt caa att act ccc cag tat gac ttt gag Asn Gly Thr Asp Glu Lys Phe Gln Ile Thr Pro Gln Tyr Asp Phe Glu 165 170 175	528
gtc ctc aga aac ctg gag cca tgg aca act tat tgt qtt caa gtt cga Val Leu Arg Asn Leu Glu Pro Trp Thr Thr Tyr Cys Val Gln Val Arg 180 185 190	576
ggg ttt ctt cct gat cgg aac aaa gct ggg gaa tgg agt gag cct gtc Gly Phe Leu Pro Asp Arg Asn Lys Ala Gly Glu Trp Ser Glu Pro Val 195 200 205	624
tgt gag caa aca acc cat gac gaa acg gtc ccc tcc gga tcc ggt teg Cys Glu Gln Thr Thr His Asp Glu Thr Val Pro Ser Gly Ser Gly Ser 210 215 220	672
agt teg ggt teg gag ccc aca tca tca gac aaa act cac aca tgc cca Gly Ser Gly Ser Glu Pro Arg Ser Ser Asp Lys Thr His Thr Cys Pro 225 230 235 240	720
ccg tgc cca gca cct gaa gct gag ggg gca ccg tca atc ttc ctc ttc Pro Cys Pro Ala Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu Phe 245 250 255	768
ccc cca aaa ccc aag gac acc ctc atg atc tcc tgg acc cct gag gtc Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Ser Thr Pro Glu Val 260 265 270	816

aca tac gta ata ata gac gta aac caa aaa gac cct gag gtc aag ttc Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe 275 280 285	364
aac tgg tac gta gac ggc gta gag gta cat aat gcc aag aca aag ccg Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro 290 295 300	912
cgg gag gag cag tac aac agc aac tac cgt gta gtc agc gtc ctc aac Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr 305 310 315 320	960
gtc ctg cac cag gac taa cta aat ggc aag gag tac aag ttc aag gtc Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val 325 330 335	1008
tcg aac aaa gcc ctc cca tcc tcc atc gag aaa acc atc tcc aaa gcc Ser Asn Lys Ala Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala 340 345 350	1056
aaa ggg cag ccc cga gaa cca cag gta tac acc ctg ccc cca tcc cgg Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg 355 360 365	1104
gat gag ctg acc aag aac cag gtc agc ctg acc tgc ctg gtc aaa ggc Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly 370 375 380	1152
ttc tat ccc agc gac atc gcc gta gag tgg gag agc aat ggg cag ccg Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro 385 390 395 400	1200
cag aac aac tac aag acc agc cct ccc ctg ctg gac tcc gac gcc tcc Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser 405 410 415	1248
ttc ttc ctc tac aac aag ctc acc ctg gac aag agc agg tgg cag cag Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln 420 425 430	1296
aaa aac atc tt tca tgc tcc gta ata at gag act ctg cac aac tac	1344

Gly Asn val Phe Ser Ser Ser val Met His Glu Ala Leu His Asn His
435 440 445

taa acg caa aag aac ctc tcc ctg tct ccg ggt aaa ctg gtt ccg cgt 1392
Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Leu Val Pro Arg
450 455 460

ggt tcc gga tca ggt aac cat cac cat cac cat cac 1428
Gly Ser Gly Ser Gly Gly His His His His His His
465 470 475

<210> 23

<211> 476

<212> PRT

<213> Homo sapiens

<400> 23

Met Ala Trp Ser Leu Gly Ser Trp Leu Gly Gly Cys Leu Leu Val Ser
1 5 10 15
Ala Leu Gly Met val Pro Pro Pro Glu Asn Val Arg Met Asn Ser Val
20 25 30
Asn Phe Lys Asn Ile Leu Gln Trp Glu Ser Pro Ala Phe Ala Lys Gly
35 40 45
Asn Leu Thr Phe Thr Ala Gln Tyr Leu Ser Tyr Arg Ile Phe Gln Asp
50 55 60
Lys Cys Met Asn Thr Thr Leu Thr Glu Cys Asp Phe Ser Ser Leu Ser
65 70 75 80
Lys Tyr Gly Asp His Thr Leu Arg Val Arg Ala Glu Phe Ala Asp Glu
85 90 95
His Ser Asp Trp Val Asn Ile Thr Phe Cys Pro Val Asp Asp Thr Ile
100 105 110
Ile Gly Pro Pro Gly Met Gln Val Glu Val Leu Asp Asp Ser Leu His
115 120 125
Met Arg Phe Leu Ala Pro Lys Ile Glu Asn Glu Tyr Glu Thr Trp Thr
130 135 140
Met Lys Asn Val Tyr Asn Ser Trp Thr Tyr Asn Val Gln Tyr Trp Lys
145 150 155 160
Asn Gly Thr Asp Glu Lys Phe Gln Ile Thr Pro Gln Tyr Asp Phe Glu
165 170 175
Val Leu Arg Asn Leu Glu Pro Trp Thr Thr Tyr Cys Val Gln Val Arg
180 185 190

Gly Phe Leu Pro Asp Arg Asn Lys Ala Gly Glu Trp Ser Ala Phe Val
 195 200 205
 Cys Glu Gln Thr Thr His Asp Glu Thr Val Pro Ser Gly Ser Gly Ser
 210 215 220
 Gly Ser Gly Ser Glu Pro Arg Ser Ser Asp Lys Thr His Thr Cys Pro
 225 230 235 240
 Pro Cys Pro Ala Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu Phe
 245 250 255
 Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
 260 265 270
 Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
 275 280 285
 Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
 290 295 300
 Arg Glu Glu Gln Lys Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
 305 310 315 320
 Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
 325 330 335
 Ser Asn Lys Ala Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala
 340 345 350
 Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
 355 360 365
 Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
 370 375 380
 Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
 385 390 395 400
 Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
 405 410 415
 Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
 420 425 430
 Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
 435 440 445
 Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Leu Val Pro Arg
 450 455 460
 Gly Ser Gly Ser Gly Gly His His His His His His
 465 470 475

<210> 24

<211> 63

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC29328

<400> 24

tcagagggat cgggttcggg ttccgggttcg gaggc aaat catcagacaa aactcaaca 60
tgc 63

<210> 25

<211> 65

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC29231

<400> 25

gaactgactc gagctactcc ataggcatat actgcgccacc tgatcctta cccggagaca 60
gggag 65

<210> 26

<211> 76

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC39335

<400> 26

atcgaattc gcagaagcca tgaggacgct gctgaccatc ttgactgtgg ggtccctggc 60
tactacgcc 70

<210> 27

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC28981

<400> 27

tttgggtc ccttacc tctt gttgaa 26

<210> 28

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer 7039043

<400> 28

ctgactcgaq ctactccata ggcataatct cggcacctga tctggaacaa cgcggaacca 60
 gtttaccgaa agacaggagag 80

<210> 29

<211> 1457

<212> DNA

<213> Artificial Sequence

<220>

<223> hcytoril extracellular cytokine binding domain
 fused to IgGgl with a Glu-Glu tag

<221> CDS

<222> (1)...(1452)

<400> 29

atg aag aag ctg ctg acc atc ttg act gtg gga tcc ctg gct gct cac 48
 Met Arg Thr Leu Leu Thr Ile Leu Thr Val Gly Ser Leu Ala Ala His
 1 5 10 15

gcc cct gaq gac ccc tgg gat ctg ctc cag cac gtg aaa ttc cag tcc 96
 Ala Pro Glu Asp Pro Ser Asp Leu Leu Gln His Val Lys Phe Gln Ser
 20 25 30

agc aac ttt gaa aac atc ctg aag tgg gac agc ggg cca gag ggc acc 144
 Ser Asn Phe Glu Asn Ile Leu Thr Trp Asp Ser Gly Pro Glu Gly Thr
 35 40 45

cca gac acg atc tac aac atc gaa tat aag aag tac gaa gaa aag gac 192
 Pro Asp Thr Val Lys Ser Ile Glu Lys Lys Thr Lys Gly Glu Arg Asp
 50 55 60

tgg gta tta aag aag ggc tat cag cag atc acc cag aag tcc tgc aac 240
 Trp Val Ala Lys Lys Gly Lys Gln Arg Ile Thr Arg Lys Ser Lys Asn
 65 70 75

ctg acc ata gaa aac gaa aac ata gaa ata ttc tac tat gac aag att Leu Thr Val Glu Ile Gly Asn Leu Thr Ala Leu Tyr Tyr Ala Arg Val 80 90 95	288
acc gct gtc aat gag gga ggc cgg tca acc acc aag atg act gac aag Thr Ala Val Ser Ala Gly Gly Arg Ser Ala Thr Lys Met Thr Asp Arg 100 105 110	336
ttc agc tct cta cag cac act acc ctc aag cca cct gat gtg acc tat Phe Ser Ser Leu Gln His Thr Thr Leu Lys Pro Pro Asp Val Thr Cys 115 120 125	384
atc tcc aaa gtg aaa tcg att cag ata att gtt cat cct acc ccc aag Ile Ser Lys Val Arg Ser Ile Gln Met Ile Val His Pro Thr Pro Thr 130 135 140	432
cca atc cgt gca ggc gat ggc cac cgg cta acc ctg gaa gac atc ttc Pro Ile Arg Ala Gly Asp Gly His Arg Leu Thr Leu Glu Asp Ile Phe 145 150 155 160	480
cat gac ctg ttc tac cac tta gag ctc cag gtc aac cgc acc tac caa His Asp Leu Phe Tyr His Leu Glu Leu Gln Val Asn Arg Thr Tyr Gln 165 170 175	528
atg cac ctt gga qqq aag cag aga gaa tat gag ttc ttc ggc ctg acc Met His Leu Gly Gly Lys Gln Arg Glu Tyr Glu Phe Phe Gly Leu Thr 180 185 190	576
cct gac aca gag ttc ctt ggc acc atc atg att tgc gtt ccc acc tgg Pro Asp Thr Glu Phe Leu Gly Thr Ile Met Ile Cys Val Pro Thr Trp 195 200 205	624
gac aag gaa aat aac ccc tac atg tgc caa gtg aag aca ctg cca gac Ala Lys Glu Ser Ala Pro Tyr Met Cys Arg Val Lys Thr Leu Pro Asp 210 215 220	672
cgg aca taa aac aca tcc ggt tcg ggt tca ggt tcg gag ccc aqa tca Arg Thr Trp Thr Gly Ser Gly Ser Gly Ser Gly Ser Glu Pro Arg Ser 225 230 235 240	720
tca gac aaa aat aac aca tgc cca aat aat aca aca tct gaa ggc aag 245 250 255 260	768

ser asp lys thr his thr	245	lys pro arg cys pro ala pro glu ala glu	255
agg gca ccg tca gtc ttc ttc ttc ccc cca aaa ccc aag gac acc ctc	260	gly ala pro ser val phe leu phe pro pro lys pro lys asp thr leu	270
atg atc tcc cgg acc cct gaa gtc aca tgc gtg gtg gtg gac gtg agc	275	met ile ser arg thr pro glu val thr cys val val val asp val ser	285
cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag	290	his glu asp pro glu val lys phe asn trp tyr val asp gly val glu	300
gtg cat aat gcc aag aca aag ccg cgg gag gag cag tac aac agc acg	305	val his asn ala lys thr lys pro arg glu glu gln tyr asn ser thr	320
tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat	325	tyr arg val val ser val leu thr val leu his gln asp trp leu asn	335
ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca tcc tcc	340	gly lys glu tyr lys cys lys val ser asn lys ala leu pro ser ser	350
atc gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag	355	ile glu lys thr ile ser lys ala lys gly gln pro arg glu pro gln	365
gtg tac acc ctg ccc cca tcc ccg gat gag ctg acc aag aac cag gtc	370	val tyr thr leu pro pro ser arg asp glu leu thr lys asn gln val	380
agc ctg acc tgc ctg gtc aaa gcc ttc tat ccc agc gac atc gcc gtg	385	ser leu thr cys leu val lys gly phe tyr pro ser asp ile ala val	400
gag tgg aag arg aat aag caa cca aag aac aac tac aag acc acg cct	405	glu trp glu ser asn gly gln pro glu asn asn tyr lys thr thr pro	415

cca atg cta gac tcc aac aac tcc ttc ttc ctc tac aac aac tcc acc 1396
 Pro Val Leu Asp Ser Arg Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
 420 425 430

gta gac aag agc agg tgg cag cag gag aac gtc ttc tca tgc tcc gtg 1344
 Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 435 440 445

atg cat gag gct ctg cag aac cag tac aag cag aag agc ctc tcc ctg 1392
 Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 450 455 460

tct ccg ggt aaa ctg gtt ccg cct ggt tcc gga tca ggt ggc gag tat 1440
 Ser Pro Gly Lys Leu Val Pro Arg Gly Ser Gly Ser Gly Gly Glu Tyr
 465 470 475 480

atg cct atg gag 1452
 Met Pro Met Glu

<210> 30

<211> 484

<212> PRT

<213> Artificial Sequence

<220>

<223> peptide encoded by the hzcytor11 extracellular
 cytokine binding domain fused to IgGg1 with a
 Glu-Glu tag of SEQ ID NO: 29

<360> 30

Met Arg Thr Leu Leu Thr Ile Leu Thr Val Gly Ser Leu Ala Ala His
 1 5 10 15
 Ala Pro Glu Asp Pro Ser Asp Leu Leu Gln His Val Lys Phe Gln Ser
 20 25 30
 Ser Asn Phe Glu Asn Ile Leu Thr Trp Asp Ser Gly Pro Glu Gly Thr
 35 40 45
 Pro Asp Thr Val Tyr Ser Ile Glu Tyr Lys Thr Tyr Gly Glu Arg Asp
 50 55 60
 Trp Val Ala Lys Lys Gly Cys Gln Arg Ile Thr Arg Lys Ser Cys Asn
 65 70 75 80

Leu Thr Val Ala Thr Gly Asp Leu Thr Glu Leu Tyr Tyr Ala Arg Val
 85 90 95
 Thr Ala Val Ser Ala Gly Gly Arg Ser Ala Thr Lys Met Thr Asp Arg
 100 105 110
 Phe Ser Ser Leu Gln His Thr Thr Leu Lys Pro Pro Asp Val Thr Cys
 115 120 125
 Ile Ser Lys Val Arg Ser Ile Gln Met Ile Val His Pro Thr Pro Thr
 130 135 140
 Pro Ile Arg Ala Gly Asp Gly His Arg Leu Thr Leu Glu Asp Ile Phe
 145 150 155 160
 His Asp Leu Phe Tyr His Leu Glu Leu Gln Val Asn Arg Thr Tyr Gln
 165 170 175
 Met His Leu Gly Gly Lys Gln Arg Glu Tyr Glu Phe Phe Gly Leu Thr
 180 185 190
 Pro Asp Thr Glu Phe Leu Gly Thr Ile Met Ile Cys Val Pro Thr Trp
 195 200 205
 Ala Lys Glu Ser Ala Pro Tyr Met Cys Arg Val Lys Thr Leu Pro Asp
 210 215 220
 Arg Thr Trp Thr Gly Ser Gly Ser Gly Ser Gly Ser Glu Pro Arg Ser
 225 230 235 240
 Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Glu
 245 250 255
 Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
 260 265 270
 Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
 275 280 285
 His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
 290 295 300
 Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
 305 310 315 320
 Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
 325 330 335
 Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ser Ser
 340 345 350
 Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
 355 360 365
 Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
 370 375 380
 Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 385 390 395 400
 Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 405 410 415

Pro Val Leu Asp Ser Arg Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
 420 425 430

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 435 440 445

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 450 455 460

Ser Pro Gly Lys Leu Val Pro Arg Gly Ser Gly Ser Gly Gly Glu Tyr
 465 470 475 480

Met Pro Met Glu

<210> 31

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC37693

<400> 31

ctccagacac ggtctacagc at

22

<210> 32

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC37449

<400> 32

gggtcagccc gaagaactca tat

23

<210> 33

<211> 199

<212> PR1

<213> Homo sapiens

<400> 33

Met Val Pro Pro Pro Glu Asn Val Arg Met Asn Ser Val Asn Phe Lys
 1 5 10 15

Asn Ile Leu Thr Trp Glu Ser Ser Ala Thr Ala Lys Val Arg Leu Thr
 1 5 10 15 20 25 30 35 40
 Phe Thr Ala Glu Tyr Leu Ser Tyr Arg Thr Phe Glu Asp Lys Val Met
 35 40 45
 Asn Thr Thr Leu Thr Glu Cys Asp Phe Ser Ser Leu Ser Lys Tyr Gly
 50 55 60
 Asp His Thr Leu Arg Val Arg Ala Glu Phe Ala Asp Glu His Ser Asp
 65 70 75 80
 Trp Val Asn Ile Thr Phe Cys Pro Val Asp Asp Thr Ile Ile Gly Pro
 85 90 95
 Pro Gly Met Glu Val Glu Val Leu Ala Asp Ser Leu His Met Arg Phe
 100 105 110
 Leu Ala Pro Lys Ile Glu Asn Glu Tyr Glu Thr Trp Thr Met Lys Asn
 115 120 125
 Val Tyr Asn Ser Trp Thr Tyr Asn Val Glu Tyr Trp Lys Asn Gly Thr
 130 135 140
 Asp Glu Lys Phe Glu Ile Thr Pro Glu Tyr Asp Phe Glu Val Leu Arg
 145 150 155 160
 Asn Leu Glu Pro Trp Thr Thr Tyr Cys Val Glu Val Arg Gly Phe Leu
 165 170 175
 Pro Asp Arg Asn Lys Ala Gly Glu Trp Ser Glu Pro Val Cys Glu Glu
 180 185 190
 Thr Thr His Asp Glu Thr Val
 195

<10> 34

<11> 211

<12> PRI

<13> Homo sapiens

<400> 34

Ser Asp Ala His Gly Thr Glu Leu Pro Ser Pro Pro Ser Val Trp Phe
 1 5 10 15
 Glu Ala Glu Phe Phe His His Ile Leu His Trp Thr Pro Ile Pro Asn
 20 25 30
 Glu Ser Glu Ser Thr Cys Tyr Glu Val Ala Leu Leu Arg Tyr Gly Ile
 35 40 45
 Glu Ser Trp Asn Ser Ile Ser Asn Cys Ser Glu Thr Leu Ser Tyr Asp
 50 55 60
 Leu Thr Ala Val Thr Leu Asp Leu Tyr His Ser Asn Gly Tyr Arg Ala
 65 70 75 80

Arg Val Arg Ala Val Arg Val Ser Arg His Ser Asn Trp Thr Val Thr
95

Asn Thr Arg Phe Ser Val Arg Ala Val Thr Leu Thr Val Gly Ser Val
100 105 110

Asn Leu Glu Ile His Asn Gly Phe Ile Leu Gly Lys Ile Gln Leu Pro
115 120 125

Arg Pro Lys Met Ala Pro Ala Asn Asp Thr Tyr Glu Ser Ile Phe Ser
130 135 140

His Phe Arg Glu Tyr Glu Ile Ala Ile Arg Lys Val Pro Gly Asn Phe
145 150 155 160

Thr Phe Thr His Lys Lys Val Lys His Glu Asn Phe Ser Leu Leu Thr
165 170 175

Ser Gly Glu Val Gly Glu Phe Cys Val Gln Val Lys Pro Ser Val Ala
180 185 190

Ser Arg Ser Asn Lys Gly Met Trp Ser Lys Glu Glu Cys Ile Ser Leu
195 200 205

Thr Arg Gln
210

<210> 35

<211> 201

<212> PRT

<213> Homo sapiens

<400> 35

Asp Glu Val Ala Ile Leu Pro Ala Pro Gln Asn Leu Ser Val Leu Ser
1 5 10 15

Thr Asn Met Lys His Leu Leu Met Trp Ser Pro Val Ile Ala Pro Gly
20 25 30

Glu Thr Val Tyr Tyr Ser Val Glu Tyr Gln Gly Glu Tyr Glu Ser Leu
35 40 45

Tyr Thr Ser His Ile Trp Ile Pro Ser Ser Trp Cys Ser Leu Thr Glu
50 55 60

Gly Pro Glu Cys Asp Val Thr Asp Asp Ile Thr Ala Thr Val Pro Tyr
65 70 75 80

Asn Leu Arg Val Arg Ala Thr Leu Gly Ser Gln Thr Ser Ala Trp Ser
85 90 95

Ile Leu Lys His Thr Phe Asn Arg Asn Ser Thr Ile Leu Thr Arg Pro
100 105 110

Gly Met Glu Ile Thr Lys Asp Gly Phe Thr Leu Val Ile Glu Leu Glu
115 120 125

Arg Gly Gly Phe Phe Thr Val Thr Val Ala Tyr Asp Arg Arg Glu
135 138 140

Pro Gly Ala Glu Glu His Val Lys Met Val Arg Ser Gly Gly Ile Pro
145 150 155 160

Val His Leu Glu Thr Met Glu Pro Gly Ala Ala Tyr Cys Val Lys Ala
165 170 175

Gln Thr Phe Val Lys Ala Ile Gly Arg Tyr Ser Ala Phe Ser Gln Thr
180 185 190

Glu Lys Val Glu Val Gln Gly Ala Ala
195 200